

Assembly

Assembly

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ASM400053v1

**Organism name:** [eukaryotic synthetic construct \(other sequences\)](#)

**Sex:** female

**BioSample:** [SAMN10411725](#)

**BioProject:** [PRJNA504496](#)

**Submitter:** University of Iowa

**Date:** 2019/01/08

**Assembly type:** na

**Assembly level:** Chromosome

**Genome representation:** full

**GenBank assembly accession:** GCA\_004000535.1 (latest)

**RefSeq assembly accession:** n/a

**RefSeq assembly and GenBank assembly identical:** n/a

**Assembly method:** SNP correction v. 1.0

**Expected final version:** yes

**Reference guided assembly:** GRCh38

**Genome coverage:** 1.0x

**Sequencing technology:** SNP correction

IDs: 2198481 [UID] 8201588 [GenBank]

**History** [\(Show revision history\)](#)

Comment

This genome was generated by simulation. We randomly generated a set of SNPs and modified the human hg38 reference genome. We used the the simulated genome to test the performance of error correction tools on heterozygous sequences.

Global statistics

|                                              |               |
|----------------------------------------------|---------------|
| Total sequence length                        | 3,245,113,536 |
| Total ungapped length                        | 3,093,780,512 |
| Gaps between scaffolds                       | 0             |
| Number of scaffolds                          | 25            |
| Scaffold N50                                 | 168,796,734   |
| Scaffold L50                                 | 8             |
| Number of contigs                            | 329           |
| Contig N50                                   | 33,548,238    |
| Contig L50                                   | 27            |
| Total number of chromosomes and plasmids     | 25            |
| Number of component sequences (WGS or clone) | 25            |

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[A comparative evaluation of hybrid error correction methods for error-prone long reads.](#)

Assembly Definition

Assembly Statistics

Global assembly definition

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Click on the table row to see sequence details in the table to the right

| Assembly Unit Name |
|--------------------|
| Primary Assembly   |
| non-nuclear        |

Assembly Unit: Primary Assembly (GCA\_004000545.1)

| Molecule name | GenBank sequence           |     | RefSeq sequence |
|---------------|----------------------------|-----|-----------------|
| Chromosome 1  | <a href="#">CP034487.1</a> | n/a | n/a             |
| Chromosome 2  | <a href="#">CP034498.1</a> | n/a | n/a             |
| Chromosome 3  | <a href="#">CP034502.1</a> | n/a | n/a             |
| Chromosome 4  | <a href="#">CP034503.1</a> | n/a | n/a             |
| Chromosome 5  | <a href="#">CP034504.1</a> | n/a | n/a             |
| Chromosome 6  | <a href="#">CP034505.1</a> | n/a | n/a             |
| Chromosome 7  | <a href="#">CP034506.1</a> | n/a | n/a             |
| Chromosome 8  | <a href="#">CP034507.1</a> | n/a | n/a             |
| Chromosome 9  | <a href="#">CP034508.1</a> | n/a | n/a             |
| Chromosome 10 | <a href="#">CP034488.1</a> | n/a | n/a             |
| Chromosome 11 | <a href="#">CP034489.1</a> | n/a | n/a             |
| Chromosome 12 | <a href="#">CP034490.1</a> | n/a | n/a             |
| Chromosome 13 | <a href="#">CP034491.1</a> | n/a | n/a             |
| Chromosome 14 | <a href="#">CP034492.1</a> | n/a | n/a             |
| Chromosome 15 | <a href="#">CP034493.1</a> | n/a | n/a             |
| Chromosome 16 | <a href="#">CP034494.1</a> | n/a | n/a             |
| Chromosome 17 | <a href="#">CP034495.1</a> | n/a | n/a             |
| Chromosome 18 | <a href="#">CP034496.1</a> | n/a | n/a             |
| Chromosome 19 | <a href="#">CP034497.1</a> | n/a | n/a             |
| Chromosome 20 | <a href="#">CP034499.1</a> | n/a | n/a             |
| Chromosome 21 | <a href="#">CP034500.1</a> | n/a | n/a             |
| Chromosome 22 | <a href="#">CP034501.1</a> | n/a | n/a             |
| Chromosome X  | <a href="#">CP034509.1</a> | n/a | n/a             |
| Chromosome Y  | <a href="#">CP034510.1</a> | n/a | n/a             |

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